

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 17, 2003, 16:09:09 ; Search time 18 Seconds

(without alignments)
1292,474 Million cell updates/sec

Title: US-09-978-309a-74

Perfect score: 1195

Sequence: 1 QEKYDSMVOSLEDVTAQFES.....KKKQSETKLQELNKVLGIRK 242

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1193	99.8	725	1 JC5016	hyaluronan recepto
2	914	76.5	631	2 JC4298	hyaluronan recepto
3	193.5	16.2	955	2 S24348	myosin heavy chain
4	193	16.2	1388	2 T13035	KLP2 protein - Aft
5	191	16.0	1410	1 A57013	early endosome ant
6	190	15.9	1690	2 T13030	microtubule bindin
7	187.5	15.7	741	2 S39082	myosin heavy chain
8	185.5	15.5	1790	2 S67593	transport protein
9	182.5	15.3	1938	2 A59293	skeletal myosin he
10	181.5	15.2	1940	1 A24922	myosin heavy chain
11	179.5	15.0	936	2 S39083	myosin heavy chain
12	179	15.0	697	2 T07111	myosin heavy chain
13	178.5	14.9	1940	1 S04090	myosin heavy chain
14	177.5	14.9	1938	1 JX0178	myosin heavy chain
15	176.5	14.8	845	2 I48176	myosin heavy chain
16	176.5	14.8	1937	2 I38055	synaptonemal compl
17	175.5	14.7	1940	2 A29320	myosin heavy chain
18	175.5	14.7	876	2 A23767	myosin heavy chain
19	175	14.6	993	2 S49461	myosin heavy chain
20	172.5	14.4	439	2 A60608	synaptonemal compl
21	172.5	14.4	864	2 B90395	paramyosin - fluke
22	170	14.2	1388	2 S74245	purine NTPase [imp
23	169	14.1	764	2 I51302	serine/threonine-S
24	169	14.1	1931	2 A59234	myosin heavy chain
25	167	14.0	2245	2 T18278	slow myosin heavy
26	166.5	13.9	1039	2 S18199	myosin heavy chain
27	166	13.9	1300	2 I53799	myosin heavy chain
28	166	13.9	1356	2 S32763	Cgl protein - huma
29	165	13.8	3187	2 JC5837	kinecltin 1 - human 36k Golgi complex

30	162.5	13.6	1164	2 T24806	hypothetical prote
31	162.5	13.6	1938	2 I49464	alpha cardiac myos
32	162	13.6	1935	2 A59286	myosin heavy chain
33	161.5	13.5	911	2 S51441	hypothetical prote
34	161.5	13.5	1938	1 S06005	myosin alpha heavy
35	161.5	13.5	1939	2 I48175	myosin heavy chain
36	161	13.5	746	2 T47237	myosin II heavy ch
37	161	13.5	1935	2 A37102	myosin beta heavy
38	160.5	13.4	4574	2 G02520	plectin - human
39	160	13.4	1679	2 S48385	hypothetical prote
40	160	13.4	1738	2 T14867	interactin - slime
41	160	13.4	1935	1 S06006	myosin beta heavy
42	160	13.4	1979	1 S03166	myosin heavy chain
43	159.5	13.3	1597	2 S68420	citron - mouse
44	158	13.2	978	2 A70387	conserved hypothet
45	158	13.2	1156	2 B70356	chromosome assemb

ALIGNMENTS

RESULT 1

JC5016

hyaluronan receptor - human

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999

C:Accession: JC5016

R:Wang, C.; Entwistle, J.; Hou, G.; Li, Q.; Turley, E.A.

Gene 174, 299-306, 1996

A:Title: The characterization of a human RHAM cDNA: Conservation of the hyaluronan-b

A:Reference number: JC5016; MIM:600936; PMID:8890751

A:Contents: breast

A:Accession: JC5016

A:Residues: 1-725 <MAN>

A:Cross-references: GB:U29343

A:Note: It is uncertain whether Met-1 or Met-196 is the initiator

C:Comment: This receptor regulates focal adhesion turnover, and regulates human breas

C:Genetics:

A:Gene: GDB:HMNR: RHAM

A:Cross-references: GDB:683209; OMIM:600936

A:Map position: 5q33.2-5qter

C:Superfamily: hyaluronan receptor

Query Match 99.8%; Score 1193; DB 1; Length 725;
Best Local Similarity 99.6%; Pred. No. 1.8e-53;
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	QEKYDSMVOSLEDVTAQFESYKALTAETEDKLENSLQEKAKAKNAEDVHOQIAT	60
DB	443	QEKYDSMVOSLEDVTAQFESYKALTAETEDKLENSLQEKAKAKNAEDVHOQIAT	502
QY	61	ESSNOEYVAMLDLDTKSAKTEKETVSLQKTTDQNLKQOEEFRQLDEEGR	120
DB	503	ESSNOEYVAMLDLDTKSAKTEKETVSLQKTTDQNLKQOEEFRQLDEEGR	562
QY	121	KAKEENTTAELTEETINKRLLYEELYNKTKPQIOLDAFEVEKQALLNEHGAQPOLNKI	180
DB	563	KAKEENTTAELTEETINKRLLYEELYNKTKPQIOLDAFEVEKQALLNEHGAQPOLNKI	622
QY	181	RDSYAKLLGHONLKOKIRHVYKLDKENSOLKSEVSKLRQAKKKQSETKLOEELNKVLG	240
DB	623	RDSYAKLLGHONLKOKIRHVYKLDKENSOLKSEVSKLRQAKKKQSETKLOEELNKVLG	682
QY	241	IK 242	
DB	683	IK 684	

RESULT 2

JC4298

hyaluronan receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 01-Dec-2000
C/Accession: J04298; A42925; A41923; S21586
R/Entrez: J; Zhang, S.; Yang, B.; Wong, C.; Li, Q.; Hall, C.L.; A.J.; Mowat, M.; G.

A/Title: Characterization of the murine gene encoding the hyaluronan receptor RHAMM.
A/Reference number: J04298; MUID:96011639; PMID:7590272
A/Accession: J04298
A/Molecule type: mRNA
A/Residues: 1-631 <ENT>
A/Cross-references: EMBL:X64550
R/Experimental source: 3T3 fibroblast

J. Cell Biol. 118, 753, 1992
A/Reference number: A42925; MUID:92348516; PMID:1639856
A/Accession: A42925
A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 155-376, 'S', 378-504, 'E', 506-631 <HAN>
A/Cross-references: GB:X64550
R/Note: authors translated the codon AGT for residue 377 as Thr and CTA for residue 507
J. Cell Biol. 117, 1343-1350, 1992

A/Title: Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motility
A/Reference number: A41923; MUID:92299690; PMID:1376732
A/Accession: A41923
A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 155-376, 'S', 378-504, 'E', 506-507, 'L', 508-630 <HAN2>
A/Cross-references: GB:X64550
A/Note: this sequence has been corrected in reference A42925
C/Comment: this protein regulates cell motility and transformation, and focal adhesion

A/Genetics:
A:Gene: rhnm
A:Mutations: 20/3; 54/2; 79/2; 137/3; 187/3; 259/2; 382/2; 431/2; 482/2; 515/3; 574/3; 625/3
C/Superfamily: hyaluronan receptor
F/Keywords: glycoprotein; receptor
F/260-382/Region: 21 residue repeats
F/516-574/Region: hyaluronan binding #status predicted
F/575-625/Region: hyaluronan binding #status predicted
F/116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (asn) (covalent) #status

Query Match
Best Local Similarity 76.5%; Score 914; DB 2; Length 631;
Matches 184; Conservative 20; Mismatches 38; Indels 0; Gaps 0;

QY 1 QEKDVSVOLEEDVTAQFESYKALTAETEDLKLENSIOEKAKNAEDVOHQIAT 60
DB 363 QEKNDPAOSLRDVTALQLESYSSTLEKEDLKLENTLQEKVAAEKSVEDVOQIITA 422
QY 61 ESSNOEYVRLDLQTSALKETKEITVSLQKTTDLQNLQOEEDFKOLEDEGR 120
DB 423 ESTNOEYVRLDLQTSALKETKEITVSLQKTTDLQNLQOEEDFKOLEDEGR 120
QY 121 KAEKETVATLPEELNKRRLYEELYNKTPFOLOLAFVEKQALLNENGAQEOILMTI 180
DB 483 TAEKENVMTLELMEKRLLYDELKTPFOLOLAFVEKQALLNENGAQEOILMTI 180
QY 181 RDSYAKLGHONLKOKIKHVKLKDENSOLKSEVSKIRCOLAKKOSKTLDEELNKVIG 240
DB 543 RDSYAKLGHONLKOKIKHVKLKDENSOLKSEVSKIRCOLAKKOSKTLDEELNKVIG 240
QY 241 IR 242
DB 603 IR 604

RESULT 3
S24348
myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C/Accession: S24348

R/Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A/Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform
A/Reference number: S24348; MUID:92309413; PMID:1377278
A/Accession: S24348
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-955 <MOO>
A/Cross-references: EMBL:M74085
C/Superfamily: myosin heavy chain; myosin motor domain homology
C/Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match
Best Local Similarity 16.2%; Score 193.5; DB 2; Length 955;
Matches 76; Conservative 53; Mismatches 106; Indels 121; Gaps 9;

QY 8 VQSLDVTYQFESYKALTAETEDLKLENSIOEKAKNAEDVOHQIAT 67
DB 226 IDNLRVKOKLEKSELMETIDLASNNEYSKAKANLEKCRILEQLSKIRKEEH 285
QY 68 VRMLDQTSALKETKEITVSLQKTTDLQNLQOEEDFKOLEDEGR 120
DB 286 QRMINDLSTQRAQLQTSSEGEYSROYEKKDALISOLSKQAFQOIEELKRLHEELIK 345
QY 107 -----EED-----FRKQLEDEGRKAEKENTTAETELTINKRLY-----EEL 145
DB 346 NALHALQSRDCCDLQYEEDEKAGELQRAKSNSEVAVQWKYETDIAIQTEEL 405
QY 146 YKTKTPFOLOL-----AFVEKQALLN-----HGAQEOILMTI 181
DB 406 EAKKKIARQDAEHEVAVNAKCALETKQRLQNEVEDLMIDVERANACARLDKQ 465
QY 182 DSYAKLGHONLK-----OKIKHVKLKDENSOLK 211
DB 466 KNFKKILAEKQKYEQLAELESORESLSTELFKMNAVEESLDHLETLKRNKILQ 525
QY 212 SEVSKLCOQAK-----KQ-----SETKQLEELNVLGIR 242
DB 526 QEISDLEQTAEGKAHLEKVKQIQIEKSEIOALEEVAESLHEEGKILRLQ 581

RESULT 4
T30335
Klp2 protein - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 02-Jun-2000
R/Bioleli, H.; Karsenti, E.; Veinos, I.
Cell 84, 49-59, 1996
A/Title: Klp2, a new Xenopus centrosomal kinesin-like protein required for centrosom
A/Reference number: Z20827; MUID:96140639; PMID:8548825
A/Accession: T30335
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1388 <BO>
A/Cross-references: EMBL:X94082; NID:91129172; PID:6213754; PIDN:CAA63826.1
C/Genetics:
C/Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology

Query Match
Best Local Similarity 16.2%; Score 193; DB 2; Length 1388;
Matches 71; Conservative 51; Mismatches 92; Indels 96; Gaps 7;

QY 9 QSLDVTYQFESYKALTAETEDLKLENSIOEKAKNAEDVOHQIAT 67
DB 1079 BELEKITEAFKQKOBALLTHEKELVEKQOISLTQVYKIMTDLTSRQKIRASNS 1138
QY 51 -----EDVOHQIATE-----SSNOEYVRLDLQTSALKETKEITVSLQKTTDLQNLQOEEDFKOLEDEGR 120
DB 1139 SSPVLPETPRTEGPNPYSEIANLQKRNMTNLEIVSELNERTSKNEITRL-----K 1192
QY 78 SALKETKEITVSLQKTTDLQNLQOEEDFKOLEDEGR 120

Db 1193 MOLCEENNRLEIOLNQGCKELKSOLENCNNVMDSDNDQKPSMDLKRLEKEVSEEM 1252
 QY 123 EKENTTA-----ELTEINKWRLLYEYLKTKRPFQIOLDA 158
 Db 1253 EKGKATEHLKQAELEETRNILCTKDSHLSNELSEIETRSLEAKAFKEKEIRSLDGC 1312
 QY 159 FEVEKQALLNEHGAEOELNKRIRDSYAKLLGHONLKOKIKHVVKLKDENSOLKSEVSKLR 218
 Db 1313 KYEETEKLSHELDMLRKQVFLAEENGKILGHONPNOKIQOYLKVKLKKENKLLSEAEKLR 1372
 QY 219 COLAKKQOSE 228
 Db 1373 IENLFLKESK 1382

RESULT 5

A57013
 early endosome antigen 1 - human
 M:Alternate names: endosome-associated protein
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A57013; S44243
 R:Mu, F.T.; Callaghan, J.M.; Steele-Mortimer, O.; Stenmark, H.; Parton, R.G.; Campbell, J. Biol. Chem. 270, 13503-13511, 1995
 A:Title: EEA1, an early endosome-associated protein. EEA1 is a conserved alpha-helical
 A:Reference number: A57013; MUID:95286647; PMID:7768953
 A:Accession: A57013
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1410 <RES>
 A:Cross-references: GB:L40157; NID:91016367; PIDN:AAA79121.1; PID:91016368
 R:Seelig, H.P.
 submitted to the EMBL Data Library. April 1994
 A:Reference number: S44243
 A:Accession: S44243
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-254, 'C', 256-257, 'HQ', 260-276, 'A', 278-283, 'A', 285-519, 'D', 521-574, 'EQ', 577-
 A:Cross-references: EMBL:X78998; NID:9475933; PIDN:CAA55632.1; PID:9475934
 C:Genetics:
 A:Gene: GDB:EEA1
 A:Cross-references: GDB:1369996
 A:Superfamily: human early endosome antigen 1
 C:Keywords: calmodulin binding; endocytosis; metal binding; peripheral membrane protein;

Query Match 16.0%; Score 191; DB 1; Length 1410;
 Best Local Similarity 27.7%; Pred. No. 0.017; Mismatches 69; Indels 74; Gaps 12;

Matches 74; Conservative 50; Mismatches 69; Indels 74; Gaps 12;
 QY 1 QEKYDSMVOSLEDTVAQFESYKALTAETEDIKLENSLSOEKAKAKNAEDVQHQ-----56
 Db 715 KEKYLSLEQKTELEGGQIK-----KLEADSLSEVAKSE-QALDLOQOQRLN 760
 QY 57 -----LTAESSNQ-----EYVRL-LDQTSALKETEKETVTSFLOKITDLOLQKQ 106
 Db 761 TDLELRATELSKQLEMEKEIVSTRDLQKRS-----EALSESIKOKLT-----KOE 806
 QY 107 EEDFKQLEDEGKRAEKENTTAETELTEINKWRLLYEYLKTKRPFQIOLDAFEVEKQAL 166
 Db 807 EE--KQLKODPFTLSQET-----KIQHEILNNRIQTTVELQVKKMEKRAL 851
 QY 167 LNEHGAEOELNKRIRDSY-----AKLLGHONLKOKIKHVVKLKDENSOLK 211
 Db 852 MTELSTVADKLSKYSDSLKSKSEFEKENOGKAAITDLETKCKELKHOLQOVOMENT-LK 910
 QY 212 SEVSKLRQOLAKKQOSEKTKLOEELNKV 238
 Db 911 -EQKELKRSLEKEKASHQKLKLELSNM 936

RESULT 6
 T13030

microtubule binding protein D-Clp-190 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
 C:Accession: T13030
 R:Lantz, V.A.; Miller, K.G.
 J. Cell Biol. 140, 897-910, 1998
 A:Title: A class VI unconventional myosin is associated with a homologue of a microtu
 A:Reference number: 217588; MUID:98139549; PMID:9472041
 A:Accession: T13030
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1690 <LAN>
 A:Cross-references: EMBL:AF041382; NID:92773362; PID:92773363; PIDN:AB96783.1
 A:Experimental source: strain Oregon R
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0020503
 C:Keywords: cytoskeleton

Query Match 15.9%; Score 190; DB 2; Length 1690;
 Best Local Similarity 27.1%; Pred. No. 0.023;
 Matches 75; Conservative 53; Mismatches 107; Indels 42; Gaps 11;

QY 2 EKYDSMVOSLEDTVAQFESYKALTAETEDIKLENSLSOEKAK-----KAKNAEDVQHQL 58
 Db 629 EDIRLEINQDLDEVTQOLNVQKADSSALDMLRQEGTEKSTLLEKTEKEIVQIKQAA 688
 QY 59 ATENNOEYVRMLDQTSALKETEKETVTSFLOKI-----TDLOLQKQOE-EDFR 111
 Db 689 KTLQDEKQLEKQISDLK-QLAQEKIVKTEKTEALNQIOLEKESIEQOALAKONELEDQ 747
 QY 112 KQLEDEEGR-----KAKEKNTTAELEIKWRLLYEELYNKT---KPFQIOLDAFEVEKQ 164
 Db 748 KKQSESEVHLQETIKQKQNTQKDLIEVSGSLKQLOQLEKTLGHEKLOALAELEKKE 807
 QY 165 ALLNEHGAEOEL-NKIRDSYAKL-----LGHONLKOKI-----KHVVKLKDENSOLK 211
 Db 808 TTIKEKEQELQLOQKSAESALKVVYQOLQOQAAASGESEKTVAKLHDEISQLK 867
 QY 212 SEVSKLRQOL-----AKKQOSE-----KLOEELNK 237
 Db 868 SOAETQSELKSTESNLKAKSKQLEPANSLEAEK 904

RESULT 7

S39082
 myosin heavy chain, embryonic - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999
 C:Accession: S39082; S24349; A30170; S01265
 R:Moore, L.A.; Arizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 submitted to the EMBL Data Library, August 1991
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization o
 A:Reference number: S39081
 A:Accession: S39082
 A:Molecule type: mRNA
 A:Residues: 1-741 <MOO>
 A:Cross-references: EMBL:M74086
 A:Experimental source: clone Cemb3
 R:Moore, L.A.; Arizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isof
 A:Reference number: S24348; MUID:92309413; PMID:1377278
 A:Accession: S24349
 A:Molecule type: mRNA
 A:Residues: 1-12,14-741 <MOO2>
 A:Cross-references: EMBL:M74086
 A:Experimental source: clone Cemb3
 R:Lagutka, A.A.; McCarthy, J.G.; Scherzinger, C.A.; Heywood, S.M.
 DNA 8, 39-50, 1989
 A:Title: Identification and developmental expression of a novel embryonic myosin heav
 A:Reference number: A30170; MUID:89210285; PMID:2707122
 A:Accession: A30170
 A:Molecule type: DNA

A;Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 146

143	EELYNKTKEPQIOLD-----	AFEVEKQALLNE-----	HGAQEQLL	177
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Db 1386 TELLEAKKKLAORLODAEEHVAVNKCAASLEKTKORLONEVEDLMIDVERTNACAL 1445
QY 178 NKIRDSYAKLLG-----HONLKO-----KIKHYVK-----LKDN 207
Db 1446 DKQORNFDRKLAEMKKHYETHEALFASOKESRSLSTEYKVKVNAEESIDOLETLKREN 1505
QY 208 SOLKSEVSKRLCOLAR-----KKO-----SETKLOEELNKVIGIK 242
Db 1506 KNLQOEISDLTEQIAEGGRHIELEKVKKOEKSELQALFEAEASLEFHEGKILRIQ 1565

RESULT 10

A24922
myosin heavy chain, skeletal muscle, embryonic - rat
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Rattus norvegicus (Norway rat)
C:date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Apr-2002
C:Accession: A24922; A22538; B24263
R:Strehler, E.E.; Strehler-Page, M.A.; Perittard, J.C.; Perittard, M.; Nadal-Ginard, B.
J. Mol. Biol. 190, 291-317, 1986
A:title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy
A:reference number: A24922; MUID:87060988; PMID:3783701
A:Accession: A24922
A:Molecule type: DNA
A:Residues: 1-1940 <STR>
A:Cross-references: GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PID:g1619328
R:Strehler, E.E.; Mahdavi, V.; Perittard, M.; Nadal-Ginard, B.
J. Biol. Chem. 260, 468-471, 1985
A:title: Intron positions are conserved in the 5' end region of myosin heavy-chain genes
A:reference number: A22538; MUID:85080119; PMID:2981212
A:Accession: A22538
A:Molecule type: DNA
A:Residues: 1-168 <ST2>
A:Cross-references: GB:I00370; GB:M10135; NID:9205580; PIDN:AAA1655.1; PID:g554476
R:Perittard, M.; Wydro, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal-Ginard, B.
J. Biol. Chem. 260, 15856-15862, 1985
A:title: Characterization of cDNA and genomic sequences corresponding to an embryonic my
A:reference number: A24263; MUID:86059474; PMID:2999140
A:Accession: B24263
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1358-1490, 'G', <PER>
A:Cross-references: GB:X03468; NID:9205573; PIDN:AAA1652.1; PID:g205574
A:Experimental source: clone PMHC-72
C:Genetics:
A:introns: 68/3; 116/3; 169/1
A:Note: the list of intron positions may be incomplete
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co
F:89-767/Domain: myosin motor domain homology <MMOT>
F:179-186/Region: nucleotide-binding motif A (P-loop)
F:549-586/Region: actin binding #status predicted
F:656-678/Region: actin binding #status predicted
F:840-1940/Domain: actin binding #status predicted <COI>
F:840-1280/Region: S2
F:1281-1940/Region: light meromyosin
F:130/Modified site: N6, N6-trimethyllysine (Lys) #status predicted
F:185/Binding site: ATP (Lys) #status predicted
F:696,706/Active site: Cys #status predicted

Query Match 15.2%; Score 181.5; DB 1; Length 1940;
Best Local Similarity 19.4%; Pred. No. 0.072;
Matches 69; Conservative 62; Mismatches 104; Indels 121; Gaps 7;

QY 8 VOSLEDVTAOFESYKALTASEIEDLKLENSLOEAKAKNAEDVOHOIILATESSNOY 67
Db 1208 IDNLRVOKLEKSEKLEIDDLSSSEVSYSKRNLEKICRLLLEOLLSARGKNEET 1267
QY 68 VMLLDLTKSALKETETKEIT-----VSFLQKITDLOLQKQOED- 109
Db 1268 QRSISELTQNSRLQTEAGELSROLEKESIVSLSRSKQAFQTOIEELKROLEEENAK 1327

QY 110 -----FRKLODEEGRAKAKENTTAELTEINKRLLVE----- 143
Db 1328 NALHALQSRHODLLREQEYEEQEGKAELOALSLANSANGVQMRKTYETDAIQRTTEL 1387
QY 144 -----ELYN-----KTK----- 150
Db 1388 EEAARKKLAORLODSEGEVAVNNAKCAASLEKTKORLOGEVEDLMVDYERANSIAALDKQ 1447
QY 151 -----PROIOLDAFEVEKQALLNPHGAOQLNKTRISYAKLLG-----HONK 194
Db 1448 RNFQVLAIEKTKCEESQALFALAKESRSLSTELFKVAYEALDQLETVKRENMLE 1507
QY 195 QKIRHVKKLDENSOLKSEVSKRLCOLAKK-----OSETKLOEELNKVIGIK 242
Db 1508 QEIADLTQIAENKRSIHELEKSRQWELKADQIOMALEAEALFHEEAKILRIQ 1563

RESULT 11

S39083
myosin heavy chain, neonatal (similarity) - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:date: 03-Feb-1994 #sequence, revision 03-Feb-1994 #text, change 20-Jun-2000
C:Accession: S39083; S24350; A26821
R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
submitted to the EMBL Data Library, August 1991
A:description: Analysis of the chicken fast myosin heavy chain family: Localization o
A:reference number: S39081
A:Accession: S39083
A:Molecule type: mRNA
A:Residues: 1-936 <MOO1>
A:Cross-references: EMBL:M74087
R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
J. Mol. Biol. 225, 1143-1151, 1992
A:title: Analysis of the chicken fast myosin heavy chain family. Localization of iso
A:reference number: S24348; MUID:92309413; PMID:1377278
A:Accession: S24350
A:Molecule type: mRNA
A:Residues: 3-466, 'Q', 468-641, 'R', 643-936 <MOO2>
A:Cross-references: EMBL:M74087
R:Morality, D.M.; Barringer, K.J.; Dodgson, J.B.; Richter, H.E.; Young, R.B.
DNA 6, 91-99, 1987
A:title: Genomic clones encoding chicken myosin heavy-chain genes.
A:reference number: A26821; MUID:87217964; PMID:3034534
A:Accession: A26821
A:Molecule type: DNA
A:Residues: 'F', 856-936 <MO>
A:Cross-references: GB:M1657; NID:g212371; PIDN:AAA48970.1; PID:g212372
C:Genetics:
A:introns: 886/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

Query Match 15.0%; Score 179.5; DB 2; Length 936;
Best Local Similarity 21.1%; Pred. No. 0.043;
Matches 75; Conservative 55; Mismatches 105; Indels 121; Gaps 11;

QY 8 VOSLEDVTAOFESYKALTASEIEDLKLENSLOEAKAKNAEDVOHOIILATESSNOY 67
Db 208 IDNLRVOKLEKSEKLEIDDLSSSEVSYSKRNLEKICRLLLEOLLSARGKNEET 267
QY 68 VMLLDLTKSALKETETKEIT-----VSFLQKITDLOLQKQOED- 106
Db 328 NALHALQSRHODLLREQEYEEQEGKAELOALSLANSANGVQMRKTYETDAIQRTTEL 387
QY 107 -----EED-----FRKLODEEGRAKAKENTTAELTEINKRLLY-----EEL 145
Db 146 YNKRTPFOIOLD-----AFEEVQALNE-----HGAOEOINKTR 181
QY 388 EEAARKKLAORLODAEEHVAVNKCAASLEKTKORLONEVEDLMIDYERANSACALDKQ 447
QY 182 DSYAKLLGHNK-----QKIKHYVKLDENSOLK 211

Db 448 KNDKILSEWKKYEEFTQAELEASOKESRSLSTELFKMNAVEESDHLTEFLKRENNLQ 507
 QY 212 SEVSKIRCOLAK-----KKO-----SEFKLOEELNKVGLIK 242
 Db 508 QETSDLETDLEEGKAIHELEKVKQIODEKSELQASLEAEASLEHEEGKILRLQ 563

RESULT 12

T07111
 MAR binding filament-like protein 1 - tomato

N:Alternate names: MFPI protein

C:Species: Lycopersicon esculentum (tomato)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000

C:Accession: T07111

R:Meier, I.; Phelan, T.; Guissem, W.; Spiker, S.; Schneider, D.

Plant Cell 8, 2105-2115, 1996

A:Title: MFPI a novel plant filament-like protein with affinity for matrix attachment re

A:Reference number: 215928; PMID:97112038; PMID:8953774

A:Accession: T07111

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-697 <MBL>

A:Cross-references: EMBL:X07861; NID:91771157; PIDN:CAA69181.1; PID:91771158

A:Experimental source: strain VFNT Cherry; young fruit

C:Genetics:

A:Gene: MFPI

C:Superfamily: hyaluronan receptor

C:Keywords: DNA binding; nuclear matrix

Query Match 15.0%; Score 179; DB 2; Length 697;
 Best Local Similarity 25.6%; Pred. No. 0.033;
 Matches 72; Conservative 57; Mismatches 96; Indels 56; Gaps 12;

QY 1 QEYDSMVSLEVTQAFESYKALIAS-----EIEDLKLNSLOEKAKKAEVDQH-- 55
 Db 427 QESLENSRSEVSDITVQLDQLRLSKLEKREYSKLQME--LETRASLQIRNIDETKHS 483
 QY 56 QILATP-----SSNOEYVRLMLDLQTSALKETEIKETIVSELOKTTDQONLQKO 106
 Db 484 ELIAALTTTKELKLTNEMHTMSDELVAVSNNRSLOTEL-VNYYKKREHTRNEKOE 542
 QY 107 -----EEDFRQLEDEGRKAKEKNTALTEELNEIKMPL-LYEEL 145
 Db 543 KTVITLLEELKFLAESQITREKELRSLEDE--LEK--AVESLDEIRNVLAAEEL 595
 QY 146 YNKTFRQIOLDAFEYKQALNEHGAQOLKINDSTAKL---GHONLKOKIKHYV 201
 Db 596 ELATSNSSLDEEREVHRQSVSEOKIQSOEAENLEDASHVLKGRERESLEKRAK-- 652
 QY 202 KIKDENSOLKSEVSKIRCOLAKKQSEFKLOEELNKVGLIK 242
 Db 653 KLEDEMAAKAGELRLRSQINSVK---AVEDEDEKVVAGEK 690

RESULT 13

S04090

myosin heavy chain 3, skeletal muscle, embryonic - human

N:Contains: myosin ATPase (EC 3.6.4.1)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002

C:Accession: S04090; S06146; S05442; S12460; S09333; A35082

R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Rubinstein, N.A.; Kelly, A.M.

Nucleic Acids Res. 17, 3591-3592, 1989

A:Title: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.

A:Reference number: S04090; PMID:89263803; PMID:2726495

A:Accession: S04090

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-1940 <EL>

A:Cross-references: EMBL:X13988; NID:934843; PIDN:CAA32167.1; PID:934844

R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Wu, Q.L.; Rajchowdhury, M.K.

A:Title: Human embryonic myosin heavy chain cDNA. Interspecies sequence conservation

A:Reference number: S06146; PMID:90033298; PMID:2806546

A:Accession: S06146

A:Residues: 774-1662, 'GT', 1665-1940 <EL>

A:Cross-references: EMBL:X13100; NID:931143; PIDN:CAA31492.1; PID:931144

R:Karsch-Mizrachi, I.; Travis, M.; Blau, H.; Levinand, L.A.

Nucleic Acids Res. 17, 6167-6179, 1989

A:Title: Expression and DNA sequence analysis of a human embryonic skeletal muscle my

A:Reference number: S05442; PMID:8936668; PMID:2771643

A:Accession: S05442

A:Molecule type: DNA

A:Residues: 856-1390, 'KK', 1393-1940 <KAR>

A:Cross-references: EMBL:X15696; NID:936504; PIDN:CAA33731.1; PID:91335313

R:Stedman, H.H.; Eller, M.; Jullian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.

J. Biol. Chem. 265, 3568-3576, 1990

A:Title: The human embryonic myosin heavy chain. Complete primary structure reveals e

A:Reference number: A35082; PMID:90154023; PMID:2303463

A:Contents: annotation; chromosomal assignment

R:Bober, E.

submitted to the EMBL Data Library, January 1989

A:Reference number: S12458

A:Accession: S12460

A:Molecule type: mRNA

A:Residues: 856-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>

A:Cross-references: EMBL:X51593; NID:929463; PIDN:CAA35942.1; PID:929464

A:Experimental source: clone gtmc-E

R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.

Eur. J. Biochem. 189, 55-65, 1990

A:Title: Identification of three developmentally controlled isoforms of human myosin

A:Reference number: S09333; PMID:90235862; PMID:1691980

A:Accession: S09333

A:Molecule type: mRNA

A:Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-125

1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOB>

A:Cross-references: EMBL:X51593

C:Genetics:

A:Gene: GDB:MW3

A:Cross-references: GDB:119443; OMIM:160720

A:Map position: 17p13.1-17p13.1

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; muscle

F:89-767/Domain: myosin motor domain homology <MOT>

F:179-186/Region: nucleotide-binding motif A (P-loop)

F:549-586/Region: actin binding #status predicted

F:656-678/Region: actin binding #status predicted

F:840-1940/Domain: coiled coil #status predicted <COI>

F:840-1280/Region: 52

F:1281-1940/Region: light meromyosin

F:130/Modified site: N6, N6-trimethyllysine (lys) #status predicted

F:185/Binding site: ATP (lys) #status predicted

F:696/706/Active site: Cys #status predicted

Query Match 14.9%; Score 178.5; DB 1; Length 1940;

Best Local Similarity 19.1%; Pred. No. 0.1;

Matches 68; Conservative 62; Mismatches 105; Indels 121; Gaps 7;

QY 8 VOSLEDTVTOFSYKALTFSEIEDLKLNSLSOEKRAKGAEDVQHOIATFESSNOY 67
 Db 1208 IDNLQVOKOKLKEKSEFKLEITDDSSMSVSKSANLEKICRTLEDLSPARGKNEI 1267
 QY 68 VMMLDLQTKSALKETEIKET-----VSFLQKTTDQONLQKOQED- 109
 Db 1268 QNLSLETLQTKRQLQTEAGELSRQLEKESIVQSRSQAFTQGTTELKRLDEENKAK 1327
 QY 110 -----FKRLDEDEGRKAKEKNTTALTEELNKMLLYE----- 143
 Db 1328 NALNALOSSRDCDLRLQVQEEQEGKAEIQRALSKANSEVAQWRKYETDAIORTEEL 1387
 QY 144 -----ELVY-----KTK----- 150
 Db 1388 EEAQEKLAQRLODSEQVAVNAKASLEKTKORLQGEVEDLMVDVERANSIAALDKQ 1447

OY 151 -----PFOIOLAFAVEKXOALLNENGAOEOINKINDSYAKILG-----HONIK 194
 Db 1448 RNPDKYLAWKTCKECSQSELESLKESSTELSTELKNAVEALDQETVKKREKNIE 1507
 OY 195 QRIKHVVKLDKENSQKSEVSKRLRQLAKK-----QSEFKLOEELNKVYGIR 242
 Db 1508 QEIADLTQEIANGKTIHELEKSRKQIELEKADIQALEEVALEHEHEKILIRIO 1563
 RESULT 14
 JX0178
 myosin heavy chain, fast skeletal muscle, adult [validated] - chicken
 N:Contains: myosin ATPase (EC 3.6.4.1)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Apr-2002
 C:Accession: PX0050; PX0051; PX0178; A26365; S02082; PM0009; S39081; S24351; S05
 R:Hayashida, M.; Maita, T.; Matsuda, G.
 J. Biochem. 110, 54-59, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: I. Sequence of the
 A:Reference number: PX0050; MUID:92041767; PMID:1939027
 A:Accession: PX0050
 A:Molecule type: protein
 A:Residues: 1-205 <HAY>
 R:Komine, Y.; Maita, T.; Matsuda, G.
 J. Biochem. 110, 60-67, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: II. Sequence of th
 A:Reference number: PX0051; MUID:92041768; PMID:1939028
 A:Accession: PX0051
 A:Molecule type: protein
 A:Residues: 206-636 <KOM>
 R:Maita, T.; Miyashita, T.; Matsuzono, K.; Tanioka, Y.; Matsuda, G.
 J. Biochem. 110, 68-74, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: III. Sequence of t
 A:Reference number: PX0052; MUID:92041769; PMID:1939029
 A:Accession: PX0052
 A:Molecule type: protein
 A:Residues: 201-213; 632-837 <MAT>
 R:Maita, T.; Yajima, E.; Nagata, S.; Miyashita, T.; Nakayama, S.; Matsuda, G.
 J. Biochem. 110, 75-87, 1991
 A>Title: The primary structure of skeletal muscle myosin heavy chain: IV. Sequence of th
 A:Reference number: JX0178; MUID:92041770; PMID:1939030
 A:Accession: JX0178
 A:Molecule type: protein
 A:Residues: 833-1938 <MA2>
 R:Maita, T.; Hayashida, M.; Tanioka, Y.; Komine, Y.; Matsuda, G.
 Proc. Natl. Acad. Sci. U.S.A. 84, 416-420, 1987
 A>Title: The primary structure of the myosin head
 A:Reference number: A26365; MUID:87092420; PMID:3467365
 A:Accession: A26365
 A:Molecule type: protein
 A:Residues: 1-129, 'X', 131-139, 141-550, 'X', 552-754, 'X', 756-784, 'QL', 787-804, 806-810 <MA3>
 R:Matanabe, B.
 Biol. Chem. Hoppe-Seyler 370, 55-61, 1989
 A>Title: Amino acid sequence of the hinge region in chicken myosin subfragment-2.
 A:Reference number: S02082; MUID:89228549; PMID:2713098
 A:Accession: S02082
 A:Molecule type: protein
 A:Residues: 1144-1270 <MAT>
 R:Yajima, E.
 Nagasaki Igakkaei Zasshi 65, 409-430, 1990
 A>Title: Study on tail region of skeletal muscle myosin: primary structure and protease
 A:Reference number: PM0009
 A:Accession: PM0009
 A:Molecule type: protein
 A:Residues: 1304-1938 <YAJ>
 R:Moore, L.A.; Arizubiete, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 Submitted to the EMBL Data Library, August 1991
 A:Description: Analysis of the chicken fast myosin heavy chain family: Localization of
 A:Reference number: S39081
 A:Accession: S39081
 A:Molecule type: mRNA
 A:Residues: 1081-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1795, 'HV', 1798-1829, 'S', 1831
 A:Cross-references: EMBL:M74084

R:Moore, L.A.; Arizubiete, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.
 J. Mol. Biol. 225, 1143-1151, 1992
 A>Title: Analysis of the chicken fast myosin heavy chain family. Localization of isofo
 A:Reference number: S24348; MUID:92309413; PMID:1377278
 A:Accession: S24351
 A:Molecule type: mRNA
 A:Residues: 1082-1182, 'T', 1184-1203, 'DV', 1206-1342, 'E', 1344-1544, 'S', 1546-1780, 'M', 17
 A:Cross-references: EMBL:M74084
 R:Matanabe, B.
 Biol. Chem. Hoppe-Seyler 370, 1027-1034, 1989
 A>Title: Complete amino-acid sequence of subfragment-2 in adult chicken skeletal musc
 A:Reference number: S05515; MUID:90121764; PMID:2610940
 A:Accession: S05515
 A:Molecule type: protein
 A:Residues: 842-906, 'Q', 908-1270 <MA3>
 R:Matanabe, B.
 Biol. Chem. Hoppe-Seyler 370, 549-558, 1989
 A>Title: Amino acid sequence of the short subfragment-2 in adult chicken skeletal mus
 A:Reference number: S04501; MUID:89374803; PMID:2775482
 A:Accession: S04501
 A:Molecule type: protein
 A:Residues: 852-906, 'Q', 908-1108 <MA2>
 R:Matsuda, G.; Maita, T.; Miyashita, T.; Hayashida, M.
 J. Protein Chem. 6, 33-46, 1987
 A>Title: Structure and function of muscle myosin.
 A:Reference number: A60877
 A:Accession: A60877
 A:Molecule type: protein
 A:Residues: 1-139, 141-205 <MA1>
 R:Guilick, J.; Kropp, K.; Robbins, J.
 J. Biol. Chem. 260, 14513-14520, 1985
 A>Title: The structure of two fast-white myosin heavy chain promoters. A comparative
 A:Reference number: A92507; MUID:86033956; PMID:2997212
 A:Accession: A24124
 A:Molecule type: DNA
 A:Residues: 'M', 1-168 <GU1>
 A:Cross-references: GB:M13512; GB:M12083; GB:M13510; NID:g212363; PIDN:AAA48966.1; PI
 R:Kropp, K.; Guilick, J.; Robbins, J.
 J. Biol. Chem. 261, 6613-6618, 1986
 A>Title: A canonical sequence organization at the 5'-end of the myosin heavy chain ge
 A:Reference number: A92587; MUID:86196091; PMID:3009465
 A:Accession: C25217
 A:Molecule type: DNA
 A:Residues: 'M', 1-56, 'T', 58-76, 'T', 78-168 <KRO>
 A:Cross-references: GB:M13515; GB:M13511; NID:g212373; PIDN:AAA48971.1; PID:g555468
 C:Comment: This is a fragment of the globular head.
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: acetylated amino end; actin binding; ATP; coiled coil; hydrolase; methyl
 F:1-1938/Product: myosin heavy chain #status experimental <MAT>
 F:89-768/Domain: myosin motor domain homology <MMOT>
 F:179-186/Region: nucleotide-binding motif A (P-loop)
 F:550-587/Region: actin binding #status predicted
 F:657-679/Region: actin binding #status predicted
 F:841-1938/Domain: coiled coil <COI>
 F:841-1289/Region: S2
 F:852-1108/Domain: short subfragment 2 <SUB2>
 F:1290-1938/Region: light meromyosin
 F:1/Modified site: acetylated amino end (Ala) #status experimental
 F:35/Modified site: N6-methyllysine (Lys) #status experimental
 F:130-551/Modified site: N6/N6, N6-trimethyllysine (Lys) #status experimental
 F:185/Binding site: ATP (Lys) #status predicted
 F:697-707/Active site: Cys #status predicted
 F:755/Modified site: 3'-methylhistidine (His) #status experimental
 Query Match 14.9%; Score 177.5; DB 1; Length 1938;
 Best Local Similarity 20.5%; Pred. No. 0.11;
 Matches 73; Conservative 55; Mismatches 107; Indels 121; Gaps 10;
 OY 8 VOSLEDVVAOFSESVYALALASEIEDKLENNSSIOEKAARAGNAEVOHQIATSESSNOBY 67
 Db 1209 IDNLDORVAKOLEKEKSELMKIDLASWESKAKANLEKWCRTLEOLSEIKRKREBON 1268
 OY 68 VRMLDLOTKSAKETEI-----KEITVS-----FLQKITDLOQLKQO----- 106

```
Db      1269 ORMIINDLMTQRLQETGEGYSROAEKEDALISQSRKOGFTQOIEELKRLHEEIKAK 1328
OY      107 -----EED---FRKQLEDEGRKAKENTTAELTEINKRRLY-----EEL 145
Db      1329 NALAHLOSARHODDLREQYEEQEKGLQALSKANSEVAQWRTKYETDAIQRTIEL 1388
OY      146 YNKKPPQIOLD-----AFEEVKQALLNE-----HGAQEQLNKIR 181
Db      1389 EEAKKKLAQRLQDAEEHVAVNAKASLEKTKQRLQNEVEDLMWYERSNAACALDKQ 1448
OY      182 DSYAKLIGHQNIK-----OKIKHVYKLDENSQLK 211
Db      1449 KNEPKILAEKKQKEETQTELEASQKESRSLSTELFKMAYEESLDHETLKRKNKIQ 1508
OY      212 SEVSKLRQOLA-----KK-----KQSETKLOELNKVLGIR 242
Db      1509 QETADLTQALAEGSKAVHELEKVKKHVEQKSELQALAEASLSHEECKIILRLQ 1564
```

RESULT 15

```
148176
synaptonemal complex protein - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 148176
R:Dobson, M.J.; Pearlman, R.E.; Karatskakis, A.; Spyropoulos, B.; Moens, P.B.
J. Cell Sci. 107, 2749-2760, 1994
A:Title: Synaptonemal complex proteins: occurrence, epitope mapping and chromosome disj
A:Reference number: 148176; MUID:95181577; PMID:7876343
A:Accession: 148176
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-845 <RES>
A:Cross-references: GB:L32978; NID:9598124; PIDN:AAC42039.1; PID:9598125
A:Genetics:
A:Gene: syn1
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Query Match      14.88; Score 176.5; DB 2; Length 845;
Best Local Similarity 23.18; Pred. No. 0.054;
Matches 79; Conservative 55; Mismatches 97; Indels 111; Gaps 14;
```

```
OY      5 DSMVQSLDEVTAQPEFYKALTASIEDLKLNSSLQ-EKAAK--AGKNAE----- 51
Db      273 DEMTKFKNNNEVKLELKTLA---EDQKLDEKKQVEKLAELQCKEQELTLLQTRK 329
OY      52 ---DVQHQLATSSNQEVVRLDLQTKSALKETEIK--ETVS-----FLQKI 96
Db      330 EVHDLERQLLVTKISDQNSKQVEELKTK--LEBEKLNKMLTASCGKLSLENNKLTQET 387
OY      97 TDLQNL-----KQGEDPRKQLEDEGR----- 120
Db      388 NDMALELKQYQEDITNSKQOERMLQOENLEKEKTHLRDELSVRKEFLQOGNEVCKL 447
OY      121 -----KAEK-----ENTTAELTEEINKMRLLYEELYNKTKPFQ----- 153
Db      448 DKSEENARSIIECEVLUKKEQMKILLENKCNLRKQAEKSKYIEELHGENKALKKKSSAES 507
OY      154 IOLDAFEVERQALLNEHGAQEQLNKIRDSY-----AKLLGHONLKQIKHVYKLDENS 208
Db      508 KQINAYEIKVKNKIQLELESARKQFOEWTDNVQKEIEVKIIEBEKLLGEVEKAKAMVDEAV 567
OY      209 QLKSEVSKLRQO-----LAKKQSEFKLOELNKVIGI 241
Db      568 KLDQKQID-LRQQKRIAEKMALEMKHKQYDKIVEERDSELGL 608
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Search completed: July 17, 2003, 16:11:17
Job time : 20 secs